

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:45 ; Search time 2351.15 Seconds
(without alignments)
182.433 Million cell updates/sec

Title: US-09-851-670-18

Perfect score: 26
Sequence: 1 ttattgtgcacatttgcacagcat 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 segs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pal: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_om: *
20: em_or: *
21: em_ov: *
22: em_pat: *
23: em_ph: *
24: em_pl: *
25: em_ro: *
26: em_sts: *
27: em_sy: *
28: em_un: *
29: em_vl: *
30: em_hlgo_hum: *
31: em_hlgo_inv: *
32: em_hlgo_rod: *
33: em_hlgo_hum: *
34: em_hlgo_inv: *
35: em_hlgo_rod: *
36: em_hlgo_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	16.4	63.1	59	6	I63544	I63544 Sequence 7
2	15.4	59.2	51	6	AX162579	AX162579 Sequence
3	15	57.7	50	6	AX162580	AX162580 Sequence
4	15	57.7	51	6	AX100915	AX100915 Sequence
5	14.6	56.2	36	6	AR136901	AR136901 Sequence
c 6	14.6	56.2	39	6	A08043	A08043 Oligonucleo
c 7	14.4	55.4	20	6	AX008459	AX008459 Sequence
c 8	14.2	54.6	39	6	AR151074	AR151074 Sequence
c 9	14.2	54.6	39	6	E15028	E15028 PCR primer
10	14.2	54.6	43	6	A67664	A67664 Sequence 84
11	14.2	54.6	43	6	AR089874	AR089874 Sequence
c 12	14.2	54.6	51	6	AX116937	AX116937 Sequence
c 13	14	53.8	27	6	E64521	E64521 Sugar-respo
c 14	14	53.8	40	6	AX055762	AX055762 Sequence
c 15	14	53.8	41	6	AR093976	AR093976 Sequence
16	14	53.8	51	6	AX165789	AX165789 Sequence
17	13.8	53.1	28	6	AX008017	AX008017 Sequence
c 18	13.8	53.1	46	6	E07961	E07961 Primer 9/1
c 19	13.8	53.1	51	6	AX118393	AX118393 Sequence
c 20	13.6	52.3	37	6	AX097677	AX097677 Sequence
c 21	13.6	52.3	37	6	AX166879	AX166879 Sequence
c 22	13.6	52.3	37	6	AX167006	AX167006 Sequence
c 23	13.6	52.3	41	6	AR093977	AR093977 Sequence
c 24	13.4	51.5	51	6	AX157611	AX157611 Sequence
c 25	13.4	51.5	51	6	AX157612	AX157612 Sequence
26	13.4	51.5	51	6	AX165413	AX165413 Sequence
27	13.4	51.5	51	9	HSR293229	HSR293229 Homo sapi
28	13.4	51.5	58	6	AR095912	AR095912 Sequence
c 29	13.4	51.5	58	6	AR095913	AR095913 Sequence
30	13.2	50.8	18	6	AX166763	AX166763 Sequence
c 31	13.2	50.8	19	6	AR072796	AR072796 Sequence
c 32	13.2	50.8	27	6	A13225	A13225 Oligonucleo
c 33	13.2	50.8	27	6	AR034038	AR034038 Sequence
c 34	13.2	50.8	27	6	AR124047	AR124047 Sequence
c 35	13.2	50.8	31	6	AX077296	AX077296 Sequence
c 36	13.2	50.8	36	6	A08027	A08027 Oligonucleo
c 37	13.2	50.8	36	6	A13194	A13194 Oligonucleo
c 38	13.2	50.8	36	6	AR034033	AR034033 Sequence
c 39	13.2	50.8	36	6	AR093966	AR093966 Sequence
c 40	13.2	50.8	36	6	AR124042	AR124042 Sequence
c 41	13.2	50.8	39	22	E11772	E11772 Synthetic
42	13.2	50.8	41	6	AX078135	AX078135 Sequence
43	13.2	50.8	41	6	AX078146	AX078146 Sequence
c 44	13.2	50.8	50	6	AX026789	AX026789 Sequence
45	13.2	50.8	51	6	AX161146	AX161146 Sequence

ALIGNMENTS

RESULT 1
I63544/c I63544 59 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 7 from patent US 5663141.
ACCESSION I63544
VERSION I63544.1 GI:2481117
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 59)
AUTHORS Kurfuerst, M., Ruebsamen, K., Schmiel, B., Koerwer, W., Schweden, J. and
Hoeffken, H. W. J. H. W. J.
TITLE Hirudin/polyalkylene glycol conjugates and hirudin muteins
JOURNAL Patent: US 5663141-A 7 02-SEP-1997;
FEATURES Location/Qualifiers
source 1..59 /organism="unknown"
BASE COUNT 22 a 14 c 15 g 8 t
ORIGIN

Matches 17: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 tttgacatcttgcagca 25
||| ||||| ||||| |||
Db 31 TGTGATCTTTATCAGACA 11

RESULT 6
A08043/c A08043 39 bp DNA PAT 05-AUG-1993
DEFINITION Oligonucleotide P(450)11beta-6.
ACCESSION A08043
VERSION A08043.1 GI:413296
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
FEATURES
source
Location/Qualifiers
1. .39
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 12 a 10 c 11 g 6 t
ORIGIN

Query Match 56.2%; Score 14.6; DB 6; Length 39;
Best Local Similarity 81.0%; Pred. No. 2.7e+04;
Matches 17: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 tatttgacatcttgcaca 22
| ||||| ||||| ||||| |
Db 27 TCTTGCCCATTTTGCGA 7

RESULT 7
AX008459 AX008459 20 bp DNA PAT 06-SEP-2000
DEFINITION Sequence 111 from Patent WO996045.
ACCESSION AX008459
VERSION AX008459.1 GI:9996010
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/db_xref="taxon:32630"
1. .20
/note="Primer P1898-, pos. 1898-1879,
primer"

BASE COUNT 4 a 4 c 6 g 6 t
ORIGIN

Query Match 55.4%; Score 14.4; DB 6; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.3e+04;
Matches 15: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 gtggacatcttgcac 21
||| ||||| ||||| |||
Db 5 GTGGCCATCTTGTCC 20

RESULT 8
AR151074/c AR151074 39 bp DNA PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 14 from patent US 6231850.
ACCESSION AR151074
VERSION AR151074.1 GI:15117124
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Location/Qualifiers
1. .39
/organism="unknown"

BASE COUNT 10 a 14 c 8 g 7 t
ORIGIN

Query Match 54.6%; Score 14.2; DB 6; Length 39;
Best Local Similarity 84.2%; Pred. No. 4.1e+04;
Matches 16: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 tggacatcttgcagca 25
||| ||||| ||||| |||
Db 33 TGGCATCTGTGCTCGCA 15

RESULT 9
E15028/c E15028 39 bp DNA PAT 28-JUL-1999
LOCUS
DEFINITION PCR primer for canine Interleukin 12 40kDa subunit cDNA.
ACCESSION E15028
VERSION E15028.1 GI:5709711
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS
None
OC Artificial sequences.
PN JP 1998036397-A/12
PD 10-FEB-1998
PF 08-NOV-1996 JP 1996296789
PR 08-NOV-1995 JP 95P 289729, 23-MAY-1996 JP 96P 128104 PI
OKANO FUMIYOSHI
PC C07K14/54, C07H21/04, C12N5/10, C12N15/09, C12P21/02, (C12N5/10, PC
C12R1:91),
PC (C12P21/02, C12R1:91);
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source
1. .39
Location/Qualifiers
1. .39
/organism="artificial sequence",
source

BASE COUNT 10 a 14 c 8 g 7 t
ORIGIN

Query Match 54.6%; Score 14.2; DB 6; Length 39;
Best Local Similarity 84.2%; Pred. No. 4.1e+04;

Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0
QY	7	tgtgcatcttgcacga	25						
Dd	33	TGTGCATCTGTGTCACGA	15						
RESULT	10								
LOCUS	A67664								
DEFINITION	Sequence 84 from Patent WO9744485.						PAT	05-MAY-1999	
ACCESSION	A67664								
VERSION	A67664.1	GI:4756527							
KEYWORDS									
SOURCE		unidentified.							
ORGANISM		unclassified.							
REFERENCE		1 (bases 1 to 43)							
AUTHORS		Goodfellow,P.N.							
TITLE		METHODS FOR IDENTIFYING A MUTATION IN A GENE OF INTEREST							
JOURNAL		Patent: WO 97/4485-A 84 27-NOV-1997;							
FEATURES		HEXAGEN TECHNOLOGY LIMITED (GB)							
source		Location/Qualifiers							
		1..43							
BASE COUNT		/organism="unidentified"							
ORIGIN		/db_xref="taxon:32644"							
	12	a	14	c	7	g	10	t	
Query Match		54.6%;	Score 14.2;	DB 6;	Length 43;				
Best Local Similarity		84.2%;	Pred. No. 4.1e+04;						
Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	5	tgtgcatcttgcacg	23						
Dd	12	TATGACCATCTTCTCCAG	30						
RESULT	11								
LOCUS	AR089874						PAT	07-SEP-2000	
DEFINITION	Sequence 156 from patent US 5994075.								
ACCESSION	AR089874								
VERSION	AR089874.1	GI:10016629							
KEYWORDS									
SOURCE		Unknown.							
ORGANISM		Unknown.							
REFERENCE		Unclassified.							
AUTHORS		1 (bases 1 to 43)							
TITLE		Goodfellow,P.N.							
JOURNAL		Methods for identifying a mutation in a gene of interest without a							
FEATURES		phenotypic guide							
source		Patent: US 5994075-A 156 30-NOV-1999;							
		Location/Qualifiers							
		1..43							
BASE COUNT		/organism="unknown"							
ORIGIN		12	a	14	c	7	g	10	t
Query Match		54.6%;	Score 14.2;	DB 6;	Length 43;				
Best Local Similarity		84.2%;	Pred. No. 4.1e+04;						
Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	5	tgtgcatcttgcacg	23						
Dd	12	TATGACCATCTTCTCCAG	30						
RESULT	12								
AXI16937/c									
AOCUS	AXI16937		51	bp	DNA		PAT	11-MAY-2001	

DEFINITION	Sequence 2060 from Patent WO0129262.
ACCESSION	AX116937
VERSION	AX116937.1
KEYWORDS	GI:1403879
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 51)
JOURNAL	Picoult-Newburg,L. and Pohl,M. Genotyping reagents, kits and methods of use thereof Patent: WO 0129262-A 2000 26-APR-2001; Orchid Biosciences, Inc. (US)
FEATURES	Location/Qualifiers
source	1..51
BASE COUNT	/organism="Homo sapiens" /db_xref="taxon:9606"
ORIGIN	16 a 14 c 8 g 12 t 1 others
Query Match	54.6%; Score 14.2; DB 6; Length 51;
Best Local Similarity	84.2%; Pred. No. 4.2e+04;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy	1 ttatctggccatcttctg 19
Db	35 TTGTGTGTCGTCATCTTACT 17
RESULT	13
E64521/c	E64521 27 bp DNA PAT 07-FEB-2001
LOCUS	Sugar-responsive enhancer in alpha-amyase gene.
DEFINITION	E64521
ACCESSION	E64521.1 GI:13017856
VERSION	JP 1999332584-A/53.
KEYWORDS	unidentified.
SOURCE	unclassified.
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 27)
AUTHORS	Yoshimi,Y.
TITLE	Sugar-responsive enhancer in alpha-amyase gene
JOURNAL	Patent: JP 1999332584-A 53 07-DEC-1999;
COMMENT	NATIONAL SCIENCE COUNCIL
OS	Artificial Sequence
PN	JP 1999332584-A/53
PD	07-DEC-1999
PF	12-MAR-1999 JP 1999109867
PR	12-MAR-1998 TW 87103633
PI	YOSHIMI YU
PC	C12N15/09,A01H1/00,C12N5/10,C12P21/02,C12N15/00,C12N5/00 CC
Strandedness:	Single;
CC	Topology: Linear;
PH	Key
FT	source 1..27
FEATURES	Location/Qualifiers
source	1..27
BASE COUNT	/organism="Artificial Sequence" /db_xref="taxon:32644"
ORIGIN	12 a 7 c 5 g 3 t
Query Match	53.8%; Score 14; DB 6; Length 27;
Best Local Similarity	77.3%; Pred. No. 5.1e+04;
Matches	17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy	1 ttatctggccatcttctg 22
Db	26 TTATTGTGTCGTCCTATCGA 5

RESULT 14

AX055762/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

AX055762 40 bp DNA

Sequence 77 from Patent WO0073348.

AX055762

AX055762.1 GI:12228874

synthetic construct.

synthetic construct

artificial sequence.

1 (bases 1 to 40)

Baker, K.P., Goddard, A., Gurney, A.L., Hebert, C., Henzel, W.,

Kabakoff, R.C., Shelton, D.L., Smith, V., Watanabe, C.K. and Wood, W.I.

Methods and compositions for inhibiting neoplastic cell growth

Patent: WO 0073348-A 77 07-DEC-2000;

Genentech, Inc. (US)

Location/Qualifiers

1..40

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="Synthetic oligonucleotide probe."

10 a 9 c 12 g 9 t

Query Match

Best Local Similarity 77.3%; Score 14; DB 6; Length 40;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY

Db

22

TGTCCCATCATCATCCACAT 1

RESULT 15

AR093976/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

AR093976 41 bp DNA

Sequence 14 from patent US 6001595.

AR093976

AR093976.1 GI:10020721

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 41)

Ilmen, M., Onnela, M. and Penttila, M.

Promoters and uses thereof

Patent: US 6001595-A 14 14-DEC-1999;

Location/Qualifiers

1..41

/organism="unknown"

16 a 6 c 8 g 11 t

Query Match

Best Local Similarity 77.3%; Score 14; DB 6; Length 41;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY

Db

25

TTAATGAGGCTATCTTATCGA 4

1 ttatgtgcatcttgcacacat 22

||||| ||||| ||||| |||||

||||| ||||| ||||| |||||

Search completed: March 9, 2002, 00:48:46
Job time: 11127 sec

THIS PAGE BLANK (USPTO)